CLAIMS

1. A method for identifying a cellular interaction in a biological system, the method comprising:

    a) providing a predictive interaction model, wherein said predictive interaction model comprises one or more training sets; and

    b) applying said predictive interaction model to said biological system to identify a high-confidence interaction,

    thereby identifying one or more cellular interactions in said biological system.

2. A method of claim 1, further comprising validating said identified cellular interaction, said validation comprising comparing said identified cellular interaction with a control cellular interaction.

3. A method of claim 2, wherein said control cellular interaction is an experimentally derived cellular interaction.

4. A method of claim 3, wherein said experimentally derived cellular interaction is identified using a yeast two-hybrid system or a co-immunoprecipitation system.

5. The method of claim 1, wherein said one or more training sets are selected from the group consisting of postive training sets, negative training sets, and non-interacting training sets, or a combination thereof.

6. A method of claim 1, wherein said predictive interaction model further comprises one or more explanatory variables.

7. The method of claim 6, wherein said explanatory variable is selected from the group consisting of co-expression of nucleic acids, sequence similarity of polypeptides, and domain similarity of polypeptides.

8. The method of claim 1, wherein said cellular interaction is a protein-protein interaction.

9. The method of claim 1, wherein said cellular interaction is a protein-nucleic acid interaction.

10. A method of identifying an interacting protein that interacts with a test protein in a biological system, the method comprising:

    a) providing a predictive interaction model, wherein said predictive interaction model comprises one or more training sets; and

    b) applying said predictive interaction model to said biological system to identify a high-confidence interaction between said test protein and said interacting protein,

    thereby identifying one or more interacting proteins.

11. The method of claim 10, wherein said interaction is validated using a yeast two-hybrid system or a co-immunoprecipitation system.

12. The polypeptide identified by the method of claim 9.

13. A method of identifying a compound that modulates a cellular pathway in a biological system, the method comprising contacting said biological system with a candidate agent, such that a high-confidence interaction between a test protein and an interacting protein is modulated, thereby identifying a compound that modulates said cellular pathway in said biological system.

14. The method of claim 13, wherein said agent increases the expression of said test protein.

15. The method of claim 13, wherein said agent decreases the expression of said test protein.

16. The method of claim 13, wherein said agent increases the expression of said interacting protein.

17. The method of claim 13, wherein said agent decreases the expression of said interacting protein.

18. The compound identified by the method of claim 13.

19. A method of claim 13, wherein said biological system comprises a transgenic animal.

20. The method of claim 19, wherein said transgenic animal is a transgenic mouse.

21. A method of identifying a compound that modulates a cellular pathway in a biological system, the method comprising:

a) providing a predictive interaction model, wherein said predictive interaction model comprises one or more training sets;

b) applying said predictive interaction model to said biological system to identify a high-confidence interaction between said test protein and said interacting protein;

c) contacting said biological system with a candidate agent, such that said high-confidence interaction between said test protein and said interacting protein is modulated, thereby identifying a compound that modulates said cellular pathway in said biological system.

22. A method of diagnosing a test subject affected by an aberrant cellular pathway, the method comprising:

a) providing a predictive interaction model, wherein said predictive interaction model comprises one or more training sets;

b) applying said predictive interaction model to a biological sample derived from said test subject to identify a first high-confidence interaction;

c) comparing said first high-confidence interaction with a second high-confidence interaction derived from a biological sample from a reference subject, wherein said reference subject is not affected by an aberrant cellular pathway, whereby a difference in said first high-confidence interaction from said second high-confidence interaction indicates that said test subject is affected by an aberrant cellular pathway.

23. A method of diagnosing a test subject suffering from or is at risk of disease or disorder characterized

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by an aberrant cellular pathway, the method comprising:

a) providing a predictive interaction model, wherein said predictive interaction model comprises one or more training sets;

b) applying said predictive interaction model to a biological sample derived from said test subject to identify a first high-confidence interaction;

c) comparing said first high-confidence interaction with a second high-confidence interaction derived from a biological sample from a reference subject, wherein said reference subject is not suffering from or at risk of disease or disorder,

whereby a difference in said first high-confidence interaction from said second high-confidence interaction indicates that said test subject suffers from or is at risk of disease or disorder.

24. The method of claim 23, wherein said disease is selected from the group consisting of a cell proliferation-associated disease, a cell differentiation-associated disease, and an apoptosis-associated disease.

25. A database comprising a predictive interaction model, wherein said predictive interaction model comprises one or more training sets.